Amendments to the Specification:

Please replace the paragraph on page 37, lines 1-16, with the following amended paragraph:

As further described in commonly owned and copending U.S. patent application serial nos. 09/774,203, filed January 29, 2001, now abandoned, and 09/632,366, filed August 3, 2000, now abandoned, and provisional U.S. patent application nos. 60/236,359, filed May 26, 2000 and 60/236,359, filed September 27, 2000, the disclosures of which are incorporated herein by reference in their entireties, "a single exon probe" comprises at least part of an exon ("reference exon") and can hybridize detectably under high stringency conditions to transcript-derived nucleic acids that include the reference exon. The single exon probe will not, however, hybridize detectably under high stringency conditions to nucleic acids that lack the reference exon but include one or more exons that are found adjacent to the reference exon in the genome.

Please replace the paragraph on page 56, lines 17-25, with the following amended paragraph:

Genome-derived single exon probes and genome-derived single exon probe microarrays have the additional utility, inter alia, of permitting high-throughput detection of splice variants of the nucleic acids of the present invention, as further described in copending and commonly owned U.S. Patent application no. 09/632,366, filed August 3,

2000, now abandoned, the disclosure of which is incorporated herein by reference in its entirety.

Please replace the paragraph on page 62, lines 7-18, with the following amended paragraph:

For example, genomic nucleic acids of the present invention can be used as amplification substrates, e.g. for preparation of genome-derived single exon probes of the present invention, described above, and further described in copending and commonly-owned U.S. patent application nos. 09/774,203, filed January 29, 2001, now abandoned, and 09/632,366, filed August 3, 2000, now abandoned, and commonly-owned and copending U.S. provisional patent application nos. 60/207,456, filed May 26, 2000, 60/234,687, filed September 21, 2000, 60/236,359, filed 27 September 2000, the disclosures of which are incorporated herein by reference in their entireties.
As another example, genomic nucleic acids of the present invention can be integrated non-homologously into the genome of somatic cells, with or

Please replace the paragraph on page 149, line 14 through page 150, line 2, with the following amended paragraph:

Briefly, bioinformatic algorithms were applied to human genomic sequence data to identify putative exons. Each of the predicted exons was amplified from genomic DNA, typically centering the putative coding sequence within a larger amplicon that

included flanking noncoding sequence. These genome-derived single exon probes were arrayed on a solid support and expression of the bioinformatically predicted exons assessed through a series of simultaneous two-color hybridizations to the genome-derived single exon microarrays. The approach and procedures are further described in detail in Penn *et al.*, "Mining the Human Genome using Microarrays of Open Reading Frames," *Nature Genetics* 26:315-318 (2000); commonly owned and copending U.S. patent application no. 09/774,203, filed January 29, 2001, now abandoned; and commonly owned and copending U.S. provisional patent application nos. 60/207,456, filed May 26, 2000, 60/234,687, filed September 21, 2000, and 60/236,359, filed September 27, 2000, the disclosures of which are incorporated herein by reference in their entireties.

Please replace the paragraph on page 150, lines 3-10, with the following amended paragraph:

Using a graphical display particularly designed to facilitate computerized query of the resulting exon-specific expression data, as further described in commonly owned and copending U.S. patent application no. 09/774,203, filed January 29, 2001, now abandoned, an exon was identified that is expressed at high levels in human heart but in none of nine other tested tissues or cell types.

Please replace the paragraph on page 150, line 23 through page 151, line 2, with the following amended paragraph:

Moving downward in the view pane, horizontal fields are presented that show expression measured for various of the amplicons in human heart ("HEA"), brain ("BRA"), adult liver ("ADU"), HeLa cells ("HEL"), lung ("LUN"), fetal liver ("FET"), HBL100 cells ("HBL"), bone marrow ("BON"), BT4 cells ("BT4"), and placenta ("PLA"). As further described in commonly owned and copending U.S. patent application no. no. 09/774,203, now abandoned, the expression relative to control (here a pool of message from 10 tissues) is shown in the original display in shades of red and green, with green indicating expression greater than control.

Please replace the paragraph on page 157, line 23 through page 158, line 7, with the following amended paragraph:

Exons 1, 3, 4, 7, 8, 9, 15, 20, 24, 31, 39, 43, and 44 of hGDMLP-1 were separately amplified and the genome-derived single-exon probes arrayed for expression analysis essentially as described in Penn *et al.*, "Mining the Human Genome using Microarrays of Open Reading Frames," *Nature Genetics* 26:315-318 (2000) and commonly owned and copending U.S. patent application no. 09/774,203, filed January 29, 2001, now abandoned, the disclosures of which are incorporated herein by reference in their entireties.